RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/553,906D
Source: IFW0
Date Processed by STIC: 1/5/07

ENTERED

IFWO

RAW SEQUENCE LISTING DATE: 01/05/2007
PATENT APPLICATION: **US/10/553,906D** TIME: 14:14:14

Input Set : **N:\efs\01_05_07\10553906_efs\ALBI-41348-sequence_ST25.txt**
Output Set: **N:\CRF4\01052007\J553906D.raw**

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     3 <110> APPLICANT: Bergman, Tomas
     4       Duan, Rui-Dong
     5       Nilsson, Ake
     7 <120> TITLE OF INVENTION: Human Alkaline Sphingomyelinase and Use Thereof
     9 <130> FILE REFERENCE: ALBI 41348
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/553,906D
C--> 12 <141> CURRENT FILING DATE: 2005-10-21
    14 <150> PRIOR APPLICATION NUMBER: US 60/320,139
    15 <151> PRIOR FILING DATE: 2003-04-24
    17 <150> PRIOR APPLICATION NUMBER: US 60/481,598
    18 <151> PRIOR FILING DATE: 2003-11-05
    20 <160> NUMBER OF SEQ ID NOS: 18
    22 <170> SOFTWARE: PatentIn version 3.4
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 458
    26 <212> TYPE: PRT
    27 <213> ORGANISM: Homo sapiens
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    36             20                  25                  30
    39 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
    40         35                  40                  45
    43 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
    44     50                  55                  60
    47 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
    48 65                  70                  75                  80
    51 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
    52                 85                  90                  95
    55 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
    56             100                 105                 110
    59 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
    60         115                 120                 125
    63 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
    64     130                 135                 140
    67 Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
    68 145                 150                 155                 160
    71 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
    72                 165                 170                 175
    75 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
    76             180                 185                 190
    79 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
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83 Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
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87 Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
88 225                 230                 235                 240
91 Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
92                  245                 250                 255
95 Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
96              260                 265                 270
99 Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
100         275                 280                 285
103 Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
104     290                 295                 300
107 Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
108 305                 310                 315                 320
111 Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
112                 325                 330                 335
115 Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
116             340                 345                 350
119 His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
120         355                 360                 365
123 Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
124     370                 375                 380
127 Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
128 385                 390                 395                 400
131 Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
132                 405                 410                 415
135 Ser Ala Leu Pro Pro Asp Ala Leu Leu Val Ala Asp Gly Pro Cys Leu
136             420                 425                 430
139 Pro Ser Leu Ser Gln Ala Lys Gly Cys Met Pro Leu Ser Pro Ala Ala
140         435                 440                 445
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155 cgctcctggc tcccggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc    120
157 tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac acccccaacc    180
159 tggacgccat ggcccgagac ggggtgaagg cacgctacat gacccccgcc tttgtcacca    240
161 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg    300
163 ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg    360
165 gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg    420
167 gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg    480
169 tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag    540
171 cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct    600
173 acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg    660
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Output Set: N:\CRF4\01052007\J553906D.raw

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175 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc    720
177 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca    780
179 aacgggctgg cgacctggtt gaattccaca agttccccaa cttcaccttc cgggacatcg    840
181 agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg    900
183 agaaggtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg    960
185 cgttccccga ggccttccac tacgccaaca accccagggt cacacccctg ctgatgtaca   1020
187 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg   1080
189 gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca   1140
191 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc   1200
193 tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc   1260
195 acacagaatc tgctcttccg cctgatgctc tgctggtcgc ggacggaccc tgcctcccca   1320
197 gcttatccca ggccagaggc tgcatgccac tgtccccggc agcgccaacc cctgcttggc   1380
199 tgttatggtg ctggtaataa gcctgcagcc caggtccaaa gcccccggcg agccggtccc   1440
201 ataaccggcc ccctgccccc gcccctgctc ctgctcctcc ccttcgggcc ccctcctcct   1500
203 gcaaaacccg ctcccgaagc ggcgctgccg tctgcagcca cgcgggggcg cgcgggagtc   1560
205 ttctgcgggc gctggaacct gcagacccgg cctcggtcag ctgggagggg cccgccccgg   1620
207 cacaaagcac ccatgggaat aaaggccaag ccgcgacagt cagcaaaaaa aaaaaaaaaa   1680
209 aaaaaaaaaa aaaaaaaaaa a                                            1701
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 18
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 3
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223 Lys Tyr
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229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
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239             20                  25                  30
242 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
243         35                  40                  45
246 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
247     50                  55                  60
250 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
251 65                  70                  75                  80
254 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
255                 85                  90                  95
258 Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
259             100                 105                 110
262 Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
263         115                 120                 125
266 Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
267     130                 135                 140
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Input Set : N:\efs\01_05_07\10553906_efs\ALBI-41348-sequence_ST25.txt
Output Set: N:\CRF4\01052007\J553906D.raw

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271 145                 150                 155                 160
274 Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
275                 165                 170                 175
278 Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
279             180                 185                 190
282 Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
283         195                 200                 205
286 Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
287     210                 215                 220
290 Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
291 225                 230                 235                 240
294 Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
295                 245                 250                 255
298 Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
299             260                 265                 270
302 Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
303         275                 280                 285
306 Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
307     290                 295                 300
310 Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
311 305                 310                 315                 320
314 Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
315                 325                 330                 335
318 Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
319             340                 345                 350
322 His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
323         355                 360                 365
326 Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
327     370                 375                 380
330 Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
331 385                 390                 395                 400
334 Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
335                 405                 410                 415
338 Ser Ala Leu Pro Pro Asp Gly Arg Pro Thr Leu Leu Pro Lys Gly Arg
339             420                 425                 430
342 Ser Ala Leu Pro Pro Ser Ser Arg Pro Leu Leu Val Met Gly Leu Leu
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347     450                 455
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351 <211> LENGTH: 1878
352 <212> TYPE: DNA
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356 <220> FEATURE:
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359 <223> OTHER INFORMATION: n is a, c, g, or t
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RAW SEQUENCE LISTING DATE: 01/05/2007
PATENT APPLICATION: US/10/553,906D TIME: 14:14:14

Input Set : N:\efs\01_05_07\10553906_efs\ALBI-41348-sequence_ST25.txt
Output Set: N:\CRF4\01052007\J553906D.raw

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     366 tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac acccccaacc    180
     368 tggacgccat ggcccgagac ggggtgaagg cacgctacat gacccccgcc tttgtcacca    240
     370 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg    300
     372 ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg    360
     374 gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg    420
     376 gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg    480
     378 tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag    540
     380 cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct    600
     382 acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg    660
     384 agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc    720
     386 acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca    780
     388 aacgggctgg cgacctggtt gaattccaca agttccccaa cttcaccttc cgggacatcg    840
     390 agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg    900
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     394 cgttccccga ggccttccac tacgccaaca accccagggt cacacccctg ctgatgtaca   1020
     396 gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg   1080
     398 gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca   1140
     400 gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc   1200
     402 tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc   1260
     404 acacagaatc tgctcttccg cctgatggaa ggcctactct cctgcccaag ggaagatctg   1320
     406 ctctcccgcc cagcagcagg cccctcctcg tgatgggact gctggggacc gtgattcttc   1380
     408 tgtctgaggt cgcataacgc cccatggctc aaggaagccg ccgggagctg cccgcaggcc   1440
     410 ctgggccggc tgtctcgctg cgatgctctg ctggtcgcgg acggaccctg cctccccagc   1500
     412 ttatcccagg ccagaggctg catgccactg tccccggcag cgccaacccc tgcttggctg   1560
     414 ttatggtgct ggtaataagc ctcgcagccc aggtccagag cccccggcga gccggtccca   1620
     416 taaccggccc cctgcccctg cccctgctcc tgctcctccc cttcgggccc cctcctcctg   1680
     418 caaaacccgc tcccgaagcg gcgctgccgt ctgcagccac gcgggggcgc gcgggagctc   1740
     420 tgcgggcgct ggaacctgca gacccggcct cggtcagctg ggaggggccc gccccggcac   1800
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     439             20                  25                  30
     442 Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
     443         35                  40                  45
     446 Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
     447     50                  55                  60
     450 Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
     451 65                  70                  75                  80
     454 Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
     455                 85                  90                  95
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 905

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10,11,12,13,14,15,17,18

VERIFICATION SUMMARY DATE: 01/05/2007
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Output Set: **N:\CRF4\01052007\J553906D.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900